RAW SEQUENCE LISTING

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Application Serial Number: _____ 09/194,164 A _____
Source: _____ IFW/6 _____
Date Processed by STIC: _____ 08/25/2005 _____

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IFW16

RAW SEQUENCE LISTING   DATE: 08/25/2005
PATENT APPLICATION: US/09/194,164A   TIME: 16:07:29

Input Set : A:\31608-20001.21.txt
Output Set: N:\CRF4\08252005\I194164A.raw

SEQUENCE LISTING
```
 4  (1) GENERAL INFORMATION:
 6      (i) APPLICANT: Dan, Michael D.
 7                    Kaplan, Howard A.
 8                    Maiti, Pradip K.
11     (ii) TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
12                              SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING
THE
13                              FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
14                              DETECTION OF CANCERS
16    (iii) NUMBER OF SEQUENCES: 30
18     (iv) CORRESPONDENCE ADDRESS:
19          (A) ADDRESSEE: Morrison & Foerster LLP
20          (B) STREET: 755 Page Mill Road
21          (C) CITY: Palo Alto
22          (D) STATE: CA
23          (E) COUNTRY: USA
24          (F) ZIP: 94304-1018
26      (v) COMPUTER READABLE FORM:
27          (A) MEDIUM TYPE: Floppy disk
28          (B) COMPUTER: IBM PC compatible
29          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
32     (vi) CURRENT APPLICATION DATA:
C--> 33          (A) APPLICATION NUMBER: US/09/194,164A
C--> 34          (B) FILING DATE: 09-Apr-1999
W--> 45          (C) CLASSIFICATION:
42    (vii) PRIOR APPLICATION DATA:
38          (A) APPLICATION NUMBER: PCT/US97/08962
39          (B) FILING DATE: 22-MAY-1997
43          (A) APPLICATION NUMBER: US 08/657,449
44          (B) FILING DATE: 22-MAY-1996
47   (viii) ATTORNEY/AGENT INFORMATION:
48          (A) NAME: Glaister, Debra J.
49          (B) REGISTRATION NUMBER: 33,888
50          (C) REFERENCE/DOCKET NUMBER: 31608-20001.21
52     (ix) TELECOMMUNICATION INFORMATION:
53          (A) TELEPHONE: (650) 813-5600
54          (B) TELEFAX: (650) 494-0792
58  (2) INFORMATION FOR SEQ ID NO: 1:
60      (i) SEQUENCE CHARACTERISTICS:
61          (A) LENGTH: 543 base pairs
62          (B) TYPE: nucleic acid
63          (C) STRANDEDNESS: double
```

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64            (D) TOPOLOGY: linear
68      (ix) FEATURE:
69            (A) NAME/KEY: CDS
70            (B) LOCATION: 1..543
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 CAAGCTATTT AGGTGACACT ATAGAATACT CAAGCTATGC ATCCAACGCG TTGGGAGCTC      60
77 TCCCATATGG TCGACCTGCA GGCGGCCGCA CTAGTGATTT CAAGCTTCAT CACTGAACAC     120
79 AGAGGACTCA CCATGGAGTT TGGGCTGAGC TGGGTTTTCC TCGTTGCTCT TTTAAGAGGT     180
81 ATCCAGTGTC AGGTGCAGCT GGTGGAGTCT GGGGGAGGCG TGGTCCAGCC TGGGAGGTCC     240
83 CTGAGACTCT CCTGTGCAGC CTCTGGATTC CCCTTCAGAA GCTTTGCTAT GCACTGGGTC     300
85 CGCCAGGCTC TAGGCAAGGG GCTGGAGTGG GTGGCAGTTA TATCATATGA TGGAAGCACT     360
87 AAATACTACG CAGACTCCGT GAAGGGGCGA TTCACCATCT CCAGAGACAC TTCCAAGAAC     420
89 ACGGTGTATC TAAAAATGAA CAGGCTGAGA ACTGAGGACA CGGCTGTCTT TTACTTGTGC     480
91 GAAAGACAGA GCCTGCTGGG TGACTATGAC CACTACTACG GNTTGGACGC TTGGGGAAAG     540
93 GGA                                                                  543
95 (2) INFORMATION FOR SEQ ID NO: 2:
97      (i) SEQUENCE CHARACTERISTICS:
98            (A) LENGTH: 179 amino acids
99            (B) TYPE: amino acid
100           (C) STRANDEDNESS: single
101           (D) TOPOLOGY: linear
107     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
109     Gln Ala Ile Val Thr Leu Asn Thr Gln Ala Met His Pro Thr Arg Trp
110     1               5                  10                  15
112     Glu Leu Ser His Met Val Asp Leu Gln Ala Ala Ala Leu Val Ile Ser
113                 20                  25                  30
115     Ser Phe Ile Thr Glu His Arg Gly Leu Thr Met Glu Phe Gly Leu Ser
116                 35                  40                  45
118     Trp Val Phe Leu Val Ala Leu Leu Arg Gly Ile Gln Cys Gln Val Gln
119         50                  55                  60
121     Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
122     65                  70                  75                  80
124     Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Arg Ser Phe Ala Met His
125                 85                  90                  95
127     Trp Val Arg Gln Ala Leu Gly Lys Gly Leu Glu Trp Val Ala Val Ile
128                 100                 105                 110
130     Ser Tyr Asp Gly Ser Thr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
131                 115                 120                 125
133     Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr Leu Lys Met
134                 130                 135                 140
136     Asn Arg Leu Arg Thr Glu Asp Thr Ala Val Phe Tyr Leu Cys Glu Arg
137     145                 150                 155                 160
139     Gln Ser Leu Leu Gly Asp Tyr Asp His Tyr Tyr Gly Leu Asp Ala Trp
140                 165                 170                 175
142     Gly Lys Gly
145 (2) INFORMATION FOR SEQ ID NO: 3:
147     (i) SEQUENCE CHARACTERISTICS:
148           (A) LENGTH: 543 base pairs
149           (B) TYPE: nucleic acid
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150          (C) STRANDEDNESS: double
151          (D) TOPOLOGY: linear
157     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
159 TCCCTTTCCC CAAGCGTCCA ANCCGTAGTA GTGGTCATAG TCACCCAGCA GGCTCTGTCT    60
161 TTCGCACAAG TAAAAGACAG CCGTGTCCTC AGTTCTCAGC CTGTTCATTT TTAGATACAC   120
163 CGTGTTCTTG GAAGTGTCTC TGGAGATGGT GAATCGCCCC TTCACGGAGT CTGCGTAGTA   180
165 TTTAGTGCTT CCATCATATG ATATAACTGC CACCCACTCC AGCCCCTTGC CTAGAGCCTG   240
167 GCGGACCCAG TGCATAGCAA AGCTTCTGAA GGGGAATCCA GAGGCTGCAC AGGAGAGTCT   300
169 CAGGGACCTC CCAGGCTGGA CCACGCCTCC CCCAGACTCC ACCAGCTGCA CCTGACACTG   360
171 GATACCTCTT AAAAGAGCAA CGAGGAAAAC CCAGCTCAGC CCAAACTCCA TGGTGAGTCC   420
173 TCTGTGTTCA GTGATGAAGC TTGAAATCAC TAGTGCGGCC GCCTGCAGGT CGACCATATG   480
175 GGAGAGCTCC CAACGCGTTG GATGCATAGC TTGAGTATTC TATAGTGTCA CCTAAATAGC  ·540
177 TTG                                                                543
179 (2) INFORMATION FOR SEQ ID NO: 4:
181     (i) SEQUENCE CHARACTERISTICS:
182          (A) LENGTH: 450 base pairs
183          (B) TYPE: nucleic acid
184          (C) STRANDEDNESS: double
185          (D) TOPOLOGY: linear
189     (ix) FEATURE:
190          (A) NAME/KEY: CDS
191          (B) LOCATION: 1..450
194     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
196 CTCGAGATGG ACATGGAGTT CCAGGCGCAG CTTCTCTTCC TCCTGCTACT CTGGCTCCCA    60
198 GATATCACCG GAGATATTGT GTTGACGCAG TCTCCAGGCA CCCTGTCTTT GTCTCCAGGG   120
200 GAAAGAGCCA CCCTCTCCTG CAGGGCCAGT CAGAGTGTTA GTAGCAGCTA CTTAGCCTGG   180
202 TACCAGCAGA AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATGGTGCATC CACCAGGGCC   240
204 ACTGGCATGC CAGACAGGTC CAGTGGCAGT GGGTCCGGGA CAGACTTCAC TCTCACCATC   300
206 AGTAGACTGG AGCCTGAAGA TTTTGCAGTG TATTACTGTC AGCAGTATGG TAGCTCACCT   360
208 CAGACACCTC AGATCACTTT CGGCGGAGGG ACCAAGGTGG AGATCAAACG AACTGTGGCT   420.
210 GCACCATCTG TCTTCATCTT CCCGCCATCT                                    450
212 (2) INFORMATION FOR SEQ ID NO: 5:
214     (i) SEQUENCE CHARACTERISTICS:
215          (A) LENGTH: 150 amino acids
216          (B) TYPE: amino acid
217          (C) STRANDEDNESS: single
218          (D) TOPOLOGY: linear
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
226   Leu Glu Met Asp Met Glu Phe Gln Ala Gln Leu Leu Phe Leu Leu Leu
227   1               5                   10                  15
229   Leu Trp Leu Pro Asp Ile Thr Gly Asp Ile Val Leu Thr Gln Ser Pro
230               20                  25                  30
232   Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
233           35                  40                  45
235   Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
236       50                  55                  60
238   Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala
239   65                  70                  75                  80
241   Thr Gly Met Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
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242                          85                  90                      95
244       Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
245                     100                 105                 110
247       Cys Gln Gln Tyr Gly Ser Ser Pro Gln Thr Pro Gln Ile Thr Phe Gly
248             115                 120                 125
250       Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
251           130                 135                 140
253       Phe Ile Phe Pro Pro Ser
254       145                 150
256 (2) INFORMATION FOR SEQ ID NO: 6:
258     (i) SEQUENCE CHARACTERISTICS:
259         (A) LENGTH: 450 base pairs
260         (B) TYPE: nucleic acid
261         (C) STRANDEDNESS: double
262         (D) TOPOLOGY: linear
268     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
270 AGATGGCGGG AAGATGAAGA CAGATGGTGC AGCCACAGTT CGTTTGATCT CCACCTTGGT       60
272 CCCTCCGCCG AAAGTGATCT GAGGTGTCTG AGGTGAGCTA CCATACTGCT GACAGTAATA      120
274 CACTGCAAAA TCTTCAGGCT CCAGTCTACT GATGGTGAGA GTGAAGTCTG TCCCGGACCC      180
276 ACTGCCACTG AACCTGTCTG GCATGCCAGT GGCCCTGGTG GATGCACCAT AGATGAGGAG      240
278 CCTGGGAGCC TGGCCAGGTT TCTGCTGGTA CCAGGCTAAG TAGCTGCTAC TAACACTCTG      300
280 ACTGGCCCTG CAGGAGAGGG TGGCTCTTTC CCCTGGAGAC AAAGACAGGG TGCCTGGAGA      360
282 CTGCGTCAAC ACAATATCTC CGGTGATATC TGGGAGCCAG AGTAGCAGGA GGAAGAGAAG      420
284 CTGCGCCTGG AACTCCATGT CCATCTCGAG                                      450
286 (2) INFORMATION FOR SEQ ID NO: 7:
288     (i) SEQUENCE CHARACTERISTICS:
289         (A) LENGTH: 34 base pairs
290         (B) TYPE: nucleic acid
291         (C) STRANDEDNESS: single
292         (D) TOPOLOGY: linear
298     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
300 TATGAAGACA CCAGGCCGAT ATTGTGTTGA CGCA                                   34
302 (2) INFORMATION FOR SEQ ID NO: 8:
304     (i) SEQUENCE CHARACTERISTICS:
305         (A) LENGTH: 26 base pairs
306         (B) TYPE: nucleic acid
307         (C) STRANDEDNESS: single
308         (D) TOPOLOGY: linear
314     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
316 TATCCGGATG CAGCCACAGT TCGTTT                                            26
318 (2) INFORMATION FOR SEQ ID NO: 9:
320     (i) SEQUENCE CHARACTERISTICS:
321         (A) LENGTH: 26 base pairs
322         (B) TYPE: nucleic acid
323         (C) STRANDEDNESS: single
324         (D) TOPOLOGY: linear
330     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
332 TATTCGGACA GGTGCAGCTG GTGGAG                                            26
334 (2) INFORMATION FOR SEQ ID NO: 10:
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336        (i) SEQUENCE CHARACTERISTICS:
337            (A) LENGTH: 27 base pairs
338            (B) TYPE: nucleic acid
339            (C) STRANDEDNESS: single
340            (D) TOPOLOGY: linear
346       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
348 TATGGATCCT GAGGAGACGG TGACCGT                                      27
350 (2) INFORMATION FOR SEQ ID NO: 11:
352        (i) SEQUENCE CHARACTERISTICS:
353            (A) LENGTH: 60 base pairs
354            (B) TYPE: nucleic acid
355            (C) STRANDEDNESS: single
356            (D) TOPOLOGY: linear
362       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
364 TATATATCCG GAGGTGGTGG ATCAGGTGGA GGTGGCTCCC AGGTGCAGCT GGTGGAGTCT  60
367 (2) INFORMATION FOR SEQ ID NO: 12:
369        (i) SEQUENCE CHARACTERISTICS:
370            (A) LENGTH: 46 base pairs
371            (B) TYPE: nucleic acid
372            (C) STRANDEDNESS: single
373            (D) TOPOLOGY: linear
379       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
381 ACCTCCGGAA CCGCCACCGC CAGAGACAGA TGGTGCAGCC ACATTC               46
383 (2) INFORMATION FOR SEQ ID NO: 13:
385        (i) SEQUENCE CHARACTERISTICS:
386            (A) LENGTH: 918 base pairs
387            (B) TYPE: nucleic acid
388            (C) STRANDEDNESS: single
389            (D) TOPOLOGY: linear
393      (ix) FEATURE:
394            (A) NAME/KEY: CDS
395            (B) LOCATION: join(1..906, 913..918)
398       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
400 GAA TTC ATG AAA AAA ACC GCT ATC GCG ATC GCA GTT GCA CTG GCT GGT   48
401 Glu Phe Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly
402  1               5                  10               15
404 TTC GCT ACC GTT GCG CAG GCC GAT ATT GTG TTG ACG CAG TCT CCA GGC   96
405 Phe Ala Thr Val Ala Gln Ala Asp Ile Val Leu Thr Gln Ser Pro Gly
406              20              25              30
408 ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC AGG GCC  144
409 Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
410          35              40              45
412 AGT CAG AGT GTT AGT AGC AGC TAC TTA GCC TGG TAC CAG CAG AAA CCT  192
413 Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
414          50              55              60
416 GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT GCA TCC ACC AGG GCC ACT  240
417 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
418 65              70              75              80
420 GGC ATG CCA GAC AGG TTC AGT GGC AGT GGG TCC GGG ACA GAC TTC ACT  288
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VERIFICATION SUMMARY   DATE: 08/25/2005
PATENT APPLICATION: **US/09/194,164A**   TIME: 16:07:30

Input Set : **A:\31608-20001.21.txt**
Output Set: **N:\CRF4\08252005\I194164A.raw**

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:40 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:45 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)